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<110> Dreher, Ingeborg  
Moll, Thomas

<120> Antagonists IL-15

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<151> 2002-10-14

<160> 30

<170> PatentIn version 3.3

<210> 1

<211> 114

<212> PRT

<213> Homo sapien

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Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
85 90 95

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Thr Ser

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35 40 45

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
50 55 60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
65 70 75 80

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
85 90 95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
100 105 110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
115 120 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys  
130 135 140

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
145 150 155 160

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
165 170 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
180 185 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 195 200 205

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
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Leu Ser Leu Ser Pro Gly Lys  
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Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val  
 35 40 45

Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val  
 50 55 60

Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp  
 65 70 75 80

Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln  
 85 90 95

Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp  
 100 105 110

Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val  
 115 120 125

Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr  
 130 135 140

Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu  
 145 150 155 160

Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr  
 165 170 175

Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr  
 180 185 190

Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr  
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Ser Phe Ser Arg Thr Pro Gly Lys  
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 35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
 50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
 65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
 85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
 100 105 110

Thr Ser Asp Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys  
 115 120 125

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 130 135 140

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 145 150 155 160

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
 165 170 175

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 180 185 190

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 195 200 205

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 210 215 220

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
 225 230 235 240

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
 245 250 255

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 260 265 270

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 275 280 285

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 290 295 300

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
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325 330 335

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
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20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
100 105 110

Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys  
115 120 125

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro  
130 135 140

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr  
145 150 155 160

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser  
165 170 175

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His  
180 185 190

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile  
195 200 205

Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn  
210 215 220

Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys  
225 230 235 240

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu  
245 250 255

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe  
260 265 270

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu  
275 280 285

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr  
290 295 300

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg  
305 310 315 320

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His  
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340 345

<210> 6  
<211> 341  
<212> DNA  
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attgatgcta ctttatatac ggaaagtgat gttcacccca gttgcaaagt aacagcaatg	120
aagtgctttc tcttgaggtt acaagttatt tcacttgagt ccggagatgc aagtattcat	180
gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tgggaatgta	240
acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg	300
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cctgaggtca cgtgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	180
tgggtacgtg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac	240
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	300
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc	360
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat	420
gagctgacca agaaccaggt cagcctgacc tgcttgggtca aaggcttcta tcccagcgac	480
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	540
gtgctggact ccgacggctc cttcttctc tacagcaagc tcaccgtgga caagagcagg	600
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	660
acgcagaaga gcctctcct gtctccgggt aaatgat	697

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agcccatag tcacatgtgt ggtgggtgat gtgagcgagg atgaccaga tgtccagatc	180
agctgggttg tgaacaacgt ggaagtacac acagctcaga cacaaccca tagagaggat	240
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ggcaaggagt tcaaagcaaa ggtcaacaac aaagacctcc cagcgcccat cgagagaacc	360
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gaagagatga ctaagaaaca ggtcactctg acctgcatgg tcacagactt catgcctgaa	480
gacatttacg tggagtggac caacaacggg aaaacagagc taaactacaa gaacactgaa	540
ccagtcctgg actctgatgg ttcttacttc atgtacagca agctgagagt ggaaaagaag	600
aactgggtgg aaagaaatag ctactcctgt tcagtgggtcc acgaggggtct gcacaatcac	660
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<211> 1047

<212> DNA

<213> artificial sequence

<220>

<223> DNA coding for fusion protein

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aagtgttttc tcttgaggtt acaagttatt tcacttgagt ccggagatgc aagtattcat	180
gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tgggaatgta	240
acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg	300
cagagttttg tacatattgt ccaaagtgtc atcaacactt cggatcccaa atctgctgac	360
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc	420
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacgtgc	480
gtggtgggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	540
gtggagggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt	600
gtggtcagcg tcttcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	660
aaggtctcca acaaagccct ccagccccc atcgagaaaa ccatctccaa agccaaaggg	720
cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac	780
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg	840
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	900
ggctccttct tctctacag caagctcacc gtggacaaga gcagggtggca gcaggggaac	960

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<210> 10  
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 aagtgctttc tcttgagatt acaagttatt tcacttgagt cgggagatgc aagtattcat 180  
 gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tgggaatgta 240  
 acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg 300  
 cagagttttg tacatattgt ccaaattgtt atcaacactt cggatcccag agggcccaca 360  
 atcaagccct gtctccatg caaatgcca gcacctaac tcttggttg accatccgtc 420  
 ttcattctcc ctccaaagat caaggatgta ctcatgatct cctgagccc catagtcaca 480  
 tgttggttg tggatgtgag cgaggatgac ccagatgtcc agatcagctg gtttgtgaac 540  
 aacgtggaag tacacacagc tcagacacaa acccatagag aggattaca cagtactctc 600  
 cgggtggtca gtgccctccc catccagcac caggactgga tgagtggcaa ggagttcaaa 660  
 tgcaagggtca acaacaaaga cctcccagcg cccatcgaga gaaccatctc aaaacccaaa 720  
 gggtcagtaa gagctccaca ggtatatgtc ttgcctccac cagaagaaga gatgactaag 780  
 aaacagggtca ctctgacctg catggtcaca gacttcatgc ctgaagacat ttacgtggag 840  
 tggaccaaca acgggaaaac agagctaaac tacaagaaca ctgaaccagt cctggactct 900  
 gatggttctt acttcatgta cagcaagctg agagtggaaa agaagaactg ggtggaaaga 960  
 aatagctact cctgttcagt ggtccacgag ggtctgcaca atcaccacac gactaagagc 1020  
 ttctcccgga ctccgggtaa atgag 1045

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 <212> DNA  
 <213> Homo sapien

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gac 63

<210> 12  
<211> 72  
<212> DNA  
<213> Homo sapien

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tctgcctcga ga 72

<210> 13  
<211> 75  
<212> DNA  
<213> Homo sapien

<400> 13  
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gcagccactc agggga 75

<210> 14  
<211> 60  
<212> DNA  
<213> Homo sapien

<400> 14  
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<210> 15  
<211> 69  
<212> DNA  
<213> Homo sapien

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gggctcgt 69

<210> 16  
<211> 40  
<212> DNA  
<213> Homo sapien

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atgtcttcat tttgggctgt ttcagtgacg ggcttcctaa 40

<210> 17

<211> 144  
 <212> DNA  
 <213> Homo sapien

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 gcagggttc ctaaaacaga agcc 144

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 <211> 74  
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 tccactgggtg acaa 74

<210> 19  
 <211> 74  
 <212> DNA  
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 tgtctccatg gtgg 74

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 <211> 36  
 <212> DNA  
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<220>  
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<400> 20  
 ctgggtgaat gtaataagtg atttgaaaaa aattga 36

<210> 21  
 <211> 37  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> oligonucleotide

<400> 21  
 gatcttcaat ttttttcaaa tcacttatta cattcac 37

<210> 22  
 <211> 111  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> oligonucleotide

<400> 22  
 ctagccacca tggagacaga cacactcctg ctatgggtac tgctgctctg ggttccaggt 60  
 tccactggtg acaactgggt gaatgtaata agtgatttga aaaaaattga a 111

<210> 23  
 <211> 111  
 <212> DNA  
 <213> artificial sequence

<220>  
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 gaccactgaa gaccactta cattattcac taaacttttt ttaacttcta g 111

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 20 25 30  
 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
 35 40 45  
 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
 50 55 60

Asn	Leu	Ile	Ile	Leu	Ala	Asn	Asn	Ser	Leu	Ser	Ser	Asn	Gly	Asn	Val	65	70	75	80
Thr	Glu	Ser	Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Asn	Ile	85	90	95	
Lys	Glu	Phe	Leu	Asp	Ser	Phe	Val	His	Ile	Val	Asp	Met	Phe	Ile	Asn	100	105	110	
Thr	Ser	Asp	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	115	120	125	
Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	130	135	140	
Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	145	150	155	160
Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	165	170	175	
Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Thr	His	180	185	190	
Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	Ala	Leu	Pro	Ile	195	200	205	
Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	210	215	220	
Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	225	230	235	240
Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	245	250	255	
Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	260	265	270	
Met	Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	275	280	285	

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr  
 290 295 300

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg  
 305 310 315 320

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His  
 325 330 335

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
 340 345

<210> 25  
 <211> 347  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> mutated Fc

<400> 25

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 20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln  
 35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu  
 50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val  
 65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile  
 85 90 95

Lys Glu Phe Leu Asp Ser Phe Val His Ile Val Gln Met Phe Ile Asn  
 100 105 110

Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys  
 115 120 125

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro  
 130 135 140

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr  
 145 150 155 160

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser  
 165 170 175

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His  
 180 185 190

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile  
 195 200 205

Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn  
 210 215 220

Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys  
 225 230 235 240

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu  
 245 250 255

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe  
 260 265 270

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu  
 275 280 285

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr  
 290 295 300

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg  
 305 310 315 320

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His  
 325 330 335

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
 340 345



<210> 26  
 <211> 1108  
 <212> DNA  
 <213> Homo sapien

<400> 26  
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 catattgatg ctactttata tacggaaagt gatgttcacc ccagttgcaa agtaacagca 180  
 atgaagtgct ttctcttgga gttacaagtt atttcacttg agtccggaga tgcaagtatt 240  
 catgatacag tagaaaatct gatcatccta gcaaacaaca gtttgtcttc taatgggaat 300  
 gtaacagaat ctggatgcaa agaattgtgag gaactggagg aaaaaaatat taaagaattt 360  
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